

# Irene L Andrulis

## List of Publications by Year in descending order

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Version: 2024-02-01

211  
papers

22,278  
citations

10986  
71  
h-index

10734  
138  
g-index

222  
all docs

222  
docs citations

222  
times ranked

24790  
citing authors

#	ARTICLE	IF	CITATIONS
1	Risks of Breast, Ovarian, and Contralateral Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. JAMA - Journal of the American Medical Association, 2017, 317, 2402.	7.4	1,898
2	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
4	Breast-Cancer Risk in Families with Mutations in <i>PALB2</i> . New England Journal of Medicine, 2014, 371, 497-506.	27.0	745
5	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
6	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
7	Breast Cancer Risk Genes " Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
8	Pathology of Breast and Ovarian Cancers among <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Results from the Consortium of Investigators of Modifiers of <i>BRCA1</i> / <i>BRCA2</i> (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	2.5	513
9	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
10	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
11	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
12	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
13	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
14	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
15	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
16	Histone H3K36 mutations promote sarcomagenesis through altered histone methylation landscape. Science, 2016, 352, 844-849.	12.6	327
17	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	21.4	309
18	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289

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19	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	1.6	270
20	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	21.4	265
21	Common Breast Cancer-Predisposition Alleles Are Associated with Breast Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>American Journal of Human Genetics</i> , 2008, 82, 937-948.	6.2	257
22	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	21.4	256
23	The Breast Cancer Family Registry: an infrastructure for cooperative multinational, interdisciplinary and translational studies of the genetic epidemiology of breast cancer. <i>Breast Cancer Research</i> , 2004, 6, R375-89.	5.0	255
24	Genome-Wide Association Study in <i>BRCA1</i> Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003212.	3.5	244
25	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	21.4	221
26	<i>RAD51</i> 135Gâ†’C Modifies Breast Cancer Risk among <i>BRCA2</i> Mutation Carriers: Results from a Combined Analysis of 19 Studies. <i>American Journal of Human Genetics</i> , 2007, 81, 1186-1200.	6.2	217
27	Germline <i>BRCA2</i> 6174delT mutations in Ashkenazi Jewish pancreatic cancer patients. <i>Nature Genetics</i> , 1997, 16, 17-18.	21.4	205
28	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	6.2	201
29	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	21.4	184
30	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
31	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Implications for Risk Prediction. <i>Cancer Research</i> , 2010, 70, 9742-9754.	0.9	169
32	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv279.	6.3	152
33	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for <i>CH</i> <i>EK</i> <i>2</i> <i>*1100delC</i> Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	1.6	152
34	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. <i>Journal of Clinical Oncology</i> , 2017, 35, 2240-2250.	1.6	152
35	Co-amplification and overexpression of <i>CDK4</i> , <i>SAS</i> and <i>MDM2</i> occurs frequently in human parosteal osteosarcomas. <i>Oncogene</i> , 1999, 18, 783-788.	5.9	146
36	<i>JAG1</i> expression is associated with a basal phenotype and recurrence in lymph node-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2008, 111, 439-448.	2.5	138

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37	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2015, 24, 5356-5366.	2.9	128
38	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
39	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. <i>Science</i> , 2018, 361, .	12.6	121
40	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
41	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016, 13, e1002105.	8.4	118
42	10-year performance of four models of breast cancer risk: a validation study. <i>Lancet Oncology</i> , The, 2019, 20, 504-517.	10.7	116
43	Tumoral Lymphocytic Infiltration and Expression of the Chemokine CXCL10 in Breast Cancers from the Ontario Familial Breast Cancer Registry. <i>Clinical Cancer Research</i> , 2013, 19, 336-346.	7.0	113
44	Germline TP53 Variants and Susceptibility to Osteosarcoma. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	109
45	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. <i>Human Molecular Genetics</i> , 2016, 25, 2256-2268.	2.9	106
46	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	3.5	105
47	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
48	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2009, 18, 4442-4456.	2.9	99
49	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	6.3	99
50	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	6.2	98
51	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	5.0	97
52	Expression of insulin-like growth factor receptor, IGF-1, and IGF-2 in primary and metastatic osteosarcoma. <i>Journal of Surgical Oncology</i> , 1998, 69, 21-27.	1.7	94
53	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	3.2	94
54	Characterization of the 12q15 <i>MDM2</i> and 12q13-14 <i>CDK4</i> amplicons and clinical correlations in osteosarcoma. <i>Genes Chromosomes and Cancer</i> , 2010, 49, 518-525.	2.8	93

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55	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
56	Breast Carcinomas Arising in Carriers of Mutations in BRCA1 or BRCA2: Are They Prognostically Different?. <i>Journal of Clinical Oncology</i> , 1999, 17, 3653-3663.	1.6	92
57	The Combination of p53 Mutation and neu/erbB-2 Amplification Is Associated With Poor Survival in Node-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2004, 22, 86-96.	1.6	90
58	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	2.9	90
59	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
60	Cancer Risks Associated With <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>Journal of Clinical Oncology</i> , 2022, 40, 1529-1541.	1.6	90
61	A Genome-Wide Scan Identifies Variants in <i>NFIB</i> Associated with Metastasis in Patients with Osteosarcoma. <i>Cancer Discovery</i> , 2015, 5, 920-931.	9.4	88
62	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. <i>Breast Cancer Research</i> , 2016, 18, 15.	5.0	88
63	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
64	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	2.4	82
65	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	1.9	81
66	MDR1 Gene Expression and Outcome in Osteosarcoma: A Prospective, Multicenter Study. <i>Journal of Clinical Oncology</i> , 2000, 18, 2685-2694.	1.6	80
67	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, <i>BRCA1</i> -like status, tumor-infiltrating immune cells and survival. <i>Oncolmmunology</i> , 2018, 7, e1509820.	4.6	80
68	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. <i>Breast Cancer Research</i> , 2012, 14, R33.	5.0	78
69	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
70	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	6.3	77
71	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	6.2	76
72	Comparison of DNA- and RNA-Based Methods for Detection of TruncatingBRCA1 Mutations. <i>Human Mutation</i> , 2002, 20, 65-73.	2.5	74

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73	A high-resolution copy-number variation resource for clinical and population genetics. <i>Genetics in Medicine</i> , 2015, 17, 747-752.	2.4	73
74	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2011, 20, 3304-3321.	2.9	68
75	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	2.4	67
76	Distinguishing luminal breast cancer subtypes by Ki67, progesterone receptor or TP53 status provides prognostic information. <i>Modern Pathology</i> , 2014, 27, 554-561.	5.5	66
77	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	6.2	59
78	Personalized Risk Assessment for Prevention and Early Detection of Breast Cancer: Integration and Implementation (PERSPECTIVE I&I). <i>Journal of Personalized Medicine</i> , 2021, 11, 511.	2.5	59
79	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2014, 16, 3416.	5.0	57
80	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	56
81	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. <i>Cancer Research</i> , 2015, 75, 2457-2467.	0.9	55
82	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
83	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	2.9	53
84	Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. <i>Genetics in Medicine</i> , 2017, 19, 30-35.	2.4	53
85	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
86	Factors Affecting Distant Disease-Free Survival for Primary Invasive Breast Cancer: Use of a Log-Normal Survival Model. <i>Annals of Surgical Oncology</i> , 2000, 7, 416-426.	1.5	51
87	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	5.1	51
88	Age-specific breast cancer risk by body mass index and familial risk: prospective family study cohort (ProF-SC). <i>Breast Cancer Research</i> , 2018, 20, 132.	5.0	51
89	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	7.1	51
90	Past recreational physical activity, body size, and all-cause mortality following breast cancer diagnosis: results from the breast cancer family registry. <i>Breast Cancer Research and Treatment</i> , 2010, 123, 531-542.	2.5	50

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91	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
92	Cohort Profile: The Breast Cancer Prospective Family Study Cohort (ProF-SC). International Journal of Epidemiology, 2016, 45, 683-692.	1.9	48
93	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	7.1	48
94	Common Variants at the 19p13.1 and <i>ZNF365</i> Loci Are Associated with ER Subtypes of Breast Cancer and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 645-657.	2.5	47
95	Preferential allelic expression can lead to reduced expression of <i>BRCA1</i> in sporadic breast cancers. , 1998, 77, 1-6.		46
96	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
97	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45
98	Rare Mutations in <i>RINT1</i> Predispose Carriers to Breast and Lynch Syndrome—“Spectrum Cancers. Cancer Discovery, 2014, 4, 804-815.	9.4	44
99	Involvement and targeted intervention of dysregulated Hedgehog signaling in osteosarcoma. Cancer, 2014, 120, 537-547.	4.1	43
100	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
101	The genomic landscape of epithelioid sarcoma cell lines and tumours. Journal of Pathology, 2016, 238, 63-73.	4.5	43
102	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
103	Perceptions of Ashkenazi Jewish breast cancer patients on genetic testing for mutations in <i>BRCA1</i> and <i>BRCA2</i> . Clinical Genetics, 2000, 57, 376-383.	2.0	42
104	Inheritance of deleterious mutations at both <i>BRCA1</i> and <i>BRCA2</i> in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	5.0	42
105	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. Breast Cancer Research, 2020, 22, 8.	5.0	41
106	Genetic Variation at 9p22.2 and Ovarian Cancer Risk for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. Journal of the National Cancer Institute, 2011, 103, 105-116.	6.3	40
107	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
108	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39



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109	Patient survival and tumor characteristics associated with CHEK2:p.I157T “ findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	5.0	39
110	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.9	39
111	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	6.2	39
112	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	2.9	38
113	Prognostic Effect of Basal-Like Breast Cancers Is Time Dependent: Evidence from Tissue Microarray Studies on a Lymph Node–Negative Cohort. <i>Clinical Cancer Research</i> , 2008, 14, 4168-4174.	7.0	37
114	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015, 97, 22-34.	6.2	37
115	Recreational Physical Activity Is Associated with Reduced Breast Cancer Risk in Adult Women at High Risk for Breast Cancer: A Cohort Study of Women Selected for Familial and Genetic Risk. <i>Cancer Research</i> , 2020, 80, 116-125.	0.9	37
116	Mutational analysis of <i>BRCA1</i> and <i>BRCA2</i> genes in Chinese ovarian cancer identifies 6 novel germline mutations. <i>Human Mutation</i> , 2000, 16, 88-89.	2.5	36
117	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228,951 Women of European Descent. <i>Journal of the National Cancer Institute</i> , 2020, 112, 295-304.	6.3	35
118	Ovarian cancer susceptibility alleles and risk of ovarian cancer in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. <i>Human Mutation</i> , 2012, 33, 690-702.	2.5	34
119	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in <i>BRCA1/2</i> Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	2.5	34
120	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	2.9	33
121	Correlation of DNA methylation levels in blood and saliva DNA in young girls of the LEGACY Girls study. <i>Epigenetics</i> , 2014, 9, 929-933.	2.7	32
122	Aberrant Hedgehog Signaling and Clinical Outcome in Osteosarcoma. <i>Sarcoma</i> , 2014, 2014, 1-9.	1.3	32
123	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
124	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	1.8	31
125	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	5.0	31
126	Genome-wide association study identifies the <i>GLDC/IL33</i> locus associated with survival of osteosarcoma patients. <i>International Journal of Cancer</i> , 2018, 142, 1594-1601.	5.1	31



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127	Elevated expression of podocalyxin is associated with lymphatic invasion, basal-like phenotype, and clinical outcome in axillary lymph node-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 137, 709-719.	2.5	30
128	Height and Body Mass Index as Modifiers of Breast Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: A Mendelian Randomization Study. <i>Journal of the National Cancer Institute</i> , 2019, 111, 350-364.	6.3	30
129	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	12.8	30
130	Expression of the multidrug resistance gene in osteosarcoma: A pilot study. <i>Journal of Orthopaedic Research</i> , 1993, 11, 396-403.	2.3	29
131	The <i>FANCM</i> :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	5.2	28
132	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. <i>Nature Communications</i> , 2021, 12, 4496.	12.8	28
133	Menacalc, a quantitative method of metastasis assessment, as a prognostic marker for axillary node-negative breast cancer. <i>BMC Cancer</i> , 2015, 15, 483.	2.6	27
134	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in <i>BRCA2</i> mutation carriers. <i>Breast Cancer Research</i> , 2015, 17, 61.	5.0	26
135	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	5.0	26
136	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for <i>BRCA1</i> pathogenic variant carriers. <i>European Journal of Human Genetics</i> , 2017, 25, 432-438.	2.8	26
137	<i>BRCA1</i> and <i>BRCA2</i> pathogenic sequence variants in women of African origin or ancestry. <i>Human Mutation</i> , 2019, 40, 1781-1796.	2.5	26
138	<i>RAD51B</i> in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	2.5	26
139	Immuno-transcriptomic profiling of extracranial pediatric solid malignancies. <i>Cell Reports</i> , 2021, 37, 110047.	6.4	26
140	Validation of Intratumoral T-bet+ Lymphoid Cells as Predictors of Disease-Free Survival in Breast Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 41-48.	3.4	25
141	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	2.5	24
142	Alcohol Consumption, Cigarette Smoking, and Risk of Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Results from The <i>BRCA1</i> and <i>BRCA2</i> Cohort Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 368-378.	2.5	24
143	Identifying actionable variants using next generation sequencing in patients with a historical diagnosis of undifferentiated pleomorphic sarcoma. <i>International Journal of Cancer</i> , 2018, 142, 57-65.	5.1	23
144	Osteosarcoma and soft-tissue sarcomas with an immune infiltrate express PD-L1: relation to clinical outcome and Th1 pathway activation. <i>Oncotimmunology</i> , 2020, 9, 1737385.	4.6	23

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145	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
146	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 308-316.	2.5	22
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